



APPLICANT: Buchbinder, Jenny ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS ; FILE REFERENCE: PA-0041 ; CURRENT APPLICATION NUMBER: US/09/976, 594 ; CURRENT FILING DATE: 2001-10-12 ; PRIOR APPLICATION NUMBER: 60/1240, 409 ; PRIOR FILING DATE: 2000-10-12 ; NUMBER OF SEQ ID NOS: 1143 ; SOFTWARE: PERL Program ; SEQ ID NO: 76 ; LENGTH: 2451 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: NAME/KEY: misc feature ; OTHER INFORMATION: Incyte ID No. 6673549 035282CB1

US-09-976-594-786

RESULT 2

US-09-833-381-1475 ; Sequence 1475, Application US/09833387

1. GENERAL INFORMATION ; Patent No. 6672186 ; APPLICANT: Robison, Keith E. ; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs ; FILE REFERENCE: 5800-119 ; CURRENT APPLICATION NUMBER: 09516, 448 ; PRIOR APPLICATION NUMBER: 09516-29 ; NUMBER OF SEQ ID NOS: 2050 ; SOFTWARE: PSESEQ for Windows Version 3.0 ; SEQ ID NO: 1475 ; LENGTH: 420 ; TYPE: DNA ; ORGANISM: Homo sapiens ; US-09-833-381-1475

Query Match 17.4% ; Score 386.4 ; DB 4 ; Length 2451 ; Best Local Similarity 58.7% ; Pred. No. 2.7e-102 ; Matches 763 ; Conservative 0 ; Mismatches 501 ; Indels 36 ; Gaps 4 ;

Qy 801 AGACAGGCAATACTCGACAAATACGACATATTCTGTGGAAAGCTGTGGACATGATG 860

Db 503 ACAGGGGATAATTAGATAATGATGATAAACAGTAAAGGAAACCCGCGAGTAAC 562

Qy 861 CACCAACGAACTTGTGACTTTGAAGAGCTTAATCTGTGACAGACTGATAAACACA 920

Db 563 GTCCCTCCACATAATGGAGATTTAGCGATTATTCATGGAAATTATCATGGGAA 622

Qy 921 TTGCTAAAGCTGGTAACTACACTATCCCTGCAAAATACTATTCTTATCATAC 980

Db 623 TTGAACTTACTCGTATATCTGCTTACTCGCTTACTCCAGTAAACATGGCATTATTA 682

Qy 981 TTGGGGGAGAGATTGTGCTGTTGGCTAACAGGGTCTGGAAAGACTGGCTTTC 1040

Db 683 AGGGAAAGAGACTTAAAGCTGTGGCAAAACGAAACTGGCATTTC 742

Query Match 17.5% ; Score 389.8 ; DB 4 ; Length 420 ; Best Local Similarity 99.5% ; Pred. No. 9.9e-104 ; Matches 391 ; Conservative 0 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;

Qy 818 GACAATAGACACTATCTTGTGAAAGCTCTGGACTGATGACCAATTCTG 877

Db 28 GTCAAAATGACACTATCTTGTGAAAGCTGTCTGGACTGATGACCAATTCTG 87

Qy 878 ACTTGTGAAAGCTTAATCTGTGAAAGACTGAACTGAACTGAACTGGTAT 937

Db 88 ACTTGTGAAAGCTTAATCTGTGAAAGACTGAACTGAACTGGTAT 147

Qy 938 ACTAAGCTTACTCCCTGCAAAATACTATCTTGTGAAAGCCAGATTG 997

Db 148 ACTAAGCTTACTCCCTGCAAAATACTATCTTGTGAAAGCCAGATTG 207

Qy 998 ATGGCTTGTGTCATAAACAGGGTCTGGAAAGACTGGGCTTTCCTCAACATTGCT 1057

Db 208 ATGGCTTGTGTCATAAACAGGTCTGGAAACACTGGTTTCTCAACATTGCT 257

Qy 1058 CATATGTCATGTCATGTCATAAACGCAACCTGCAACGAAACAGATGT 1117

Db 268 CATATGTCATGTCATGTCATAAACGTCGTTTAAGAGTCAGAAACAGATGT 327

Qy 1118 ATTATGTAAGCAACCTGAAAGTTTAAAGCTGCAACGAAATT 1177

Db 328 ATTATGTAAGCAACCTGAAAGTTTAAAGCTGCAACGAAATT 387

Qy 1178 TCTTGTGAACTGTGTAAGAGCTGTGTATA 1210

Db 388 TCTTGTGAACTGTGTAAGAGCTGTGTATA 420

Qy 1434 AGCGCCTAACCCCTTGTGTCAGTGCACATTTCAGGAAATTAAAGGTGGCTGCAG 1493

Db 1163 TTGTCACCATGATGTCATTCTGTGTCAGTGCACATTTCAGGAAATAAGATCTGGCTG 1222

Qy 1494 ATTTTTAAAGTCAAATTATCTGTGTGTGTCAGTGCACATTTCAGGAA 1553

Db 1223 ACTTTGGATAA---TATATCTTGTGTCAGTGCACATTTCAGGAA 1279

RESULT 3

US-09-976-594-786

1. Sequence 786, Application US/09976594

2. Patent No. 6673549

3. GENERAL INFORMATION :

APPLICANT: Furness, Michael

Sequence 1384,	AP
Sequence 19,	APP
Sequence 788,	APP
Sequence 1425,	AP
Sequence 1,	APP
Sequence 3515,	AP
Sequence 816,	APP
Sequence 29,	APP
Sequence 3206,	AP
Sequence 126,	APP

4. - 9	573	4	US-09-702-705-1384
4. - 9	573	4	US-09-736-577-1384
4. - 9	573	4	US-09-161-24B-1384
4. - 9	573	4	US-09-671-325-1384
4. - 9	573	4	US-09-671-11E-1384
4. - 9	7905	4	US-09-976-594-1422
4. - 9	1587	4	US-09-134-001C-142
4. - 9	1245	3	US-09-118-443-1
4. - 9	1365	4	US-09-543-1354
4. - 9	1368	4	US-09-13-001C-816
4. - 9	66985	4	US-09-596-0002-29
4. - 9	2667	4	US-09-113-2344A-120
4. - 9	490	4	US-09-22-575-126
4. - 9	490	4	US-09-89-651-126
4. - 9	490	4	US-09-620-451B-126
4. - 9	490	4	US-09-139-338-126
4. - 9	490	4	US-09-504-287A-126
4. - 9	490	4	US-09-504-287B-126

ATTACHMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries						
SUMMARIES						
Result No.	Score	Query Length	DB ID	DB	Length	Match
1	493	22.2	504	4	US-09-6211-976-2923	
2	389.8	17.5	420	4	US-09-8333-381-1475	
3	386.4	17.4	2451	4	US-09-976-594-786	
4	386.4	17.2	2319	3	US-09-058-489-90	
5	383.2	17.2	4416	3	US-09-058-489-17	
6	369.4	16.6	3408	3	US-09-058-489-14	
7	369.4	16.6	5322	3	US-09-058-489-13	
8	158.2	7.1	2365	3	US-09-183-706-42	
9	158.2	7.1	2365	4	US-09-567-995-42	
10	129.4	5.8	1191	4	US-09-328-520-519	
11	129	5.8	3760	4	US-09-976-594-213	
12	127.6	5.7	1410	4	US-09-543-681A-1401	
C 13	125.6	5.6	1830121	4	US-09-557-894-1	
C 14	125.6	5.6	1830121	4	US-09-643-990A-1	
C 15	123.6	5.6	1254	5	PCT/US96-53320A-894	
C 16	123.6	5.6	1830121	4	US-09-557-884-1	
C 17	123.6	5.6	1830121	4	US-09-643-990A-1	
C 18	116.8	5.3	3230	4	US-09-961-527-03	
C 19	115.2	5.2	3347	4	US-09-702-705-318	
C 20	115.2	5.2	3347	4	US-09-736-457-118	
C 21	115.2	5.2	3347	4	US-09-614-124B-318	
C 22	115.2	5.2	3347	4	US-09-671-325-218	
C 23	115.2	5.2	3347	4	US-09-589-184-318	
C 24	115.2	5.2	3825	3	US-09-208-742-3	
C 25	113.4	5.1	1317	4	US-09-543-681A-195	
C 26	110.4	5.0	45613	4	US-09-596-002-22	

RESULT 2

1 Sequence 1475, Application US/09833384

2 *bad* *bad*

Qy 1135 TCGGAAATTGGTCAACCCAGATTATTGGGAAAGAAATTCTTGGACTTGT 11.94  
 Db 361 TCGGAAATTGGTCAACCCAGATTATTGGGAAAGAAATTCTTGGACTTGT 420

Qy 1195 AGAGCTCTTGTATATGGGGAAACCAAGTGGACATTCAATTGAGAAATAGCA 1254  
 Db 421 AGAGCTCTTGTATATGGGGAAACCAAGTGGACATTCAATTGAGAAATAGCA 479

Qy 1255 AGCTGTAAATATATATGTGCTAT 1279  
 Db 480 AGCTGTAAATATGTGCTAT 504

Query Match 17.5%; Score 389.8; DB 4; Length 420;  
 Best Local Similarity 99.5%; Pred. No. 9.e-104;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 818 GCAATAAGGAACTATCTTGTGGAACTTCTGCAAGCCTGCAACCAATTCTG 877  
 Db 28 GTCAATAATGGAACTATCTTGTGGAACTTCTGCAAGCCTGCAACCAATTCTG 87

Qy 878 ACTTTGAGAAAGTAAATCTCTGCAAGCCTGAACTTCTGCAACCAATTCTG 937  
 Db 88 ACTTTGAGAAAGTAAATCTCTGCAAGCCTGAACTTCTGCAACCAATTCTG 147

Qy 938 ACTAAGCTTACTCTGTCGCAAAATAACAGTAACTCTCATACCTGGGGAGATTG 997  
 Db 148 ACTAAGCTTACTCTGTCGCAAAATAACAGTAACTCTCATACCTGGGGAGATTG 207

Qy 998 ATGGGTTGTGCTCAAACACGGCTCTGGGAAAGACTGGGGTTCTCTACATTGGCT 1057  
 Db 208 ATGGGTTGTGCTCAAACACGGCTCTGGGAAAGCTGGGGTTCTCTACATTGGCT 267

Qy 1058 CATATGATGATGGGATAACTCCGTCGTTTAAGAGTGGGGAAACCAAGGTGT 1117  
 Db 268 CATATGATGATGGGATAACTCCGTCGTTTAAGAGTGGGGAAACCAAGGTGT 327

Qy 1118 ATTATGTCGACCAACTCGAGAACTGGTCACCCAGATTATTGGAGCCAGAAATT 1177  
 Db 328 ATTATGTCGACCAACTCGAGAACTGGTCACCCAGATTATTGGAGCCAGAAATT 387

Qy 1178 TCTTGGGACTTGTGTTAGAGTGGCTTCAACCAAGTTATTGGAGCTGGTTATA 1210  
 Db 388 TCTTGGGACTTGTGTTAGAGTGGCTTCAACCAAGTTATTGGAGCTGGTTATA 420

Query Match 17.4%; Score 386.4; DB 4; Length 2451;  
 Best Local Similarity 58.7%; Pred. No. 2.7e-102;  
 Matches 763; Conservative 0; Mismatches 501; Indels 36; Gaps 4;

Qy 801 AGCAGGGATAAACCTTGACAAATAAGCACATATTCCTGGAAGTGTCTGACATGATG 860  
 Db 503 ACACGGGATTAACTTGAGAAATACTGATGATAACCTAGTAGGGAAACCCGCAACT 562

Qy 861 CACCAACCGCAATTCTGACTTTGAGAAGCTTACTCTGTCGAACACTGATAACACA 920  
 Db 563 GTCTCCACATATGGAAATTCTGACATGGGAAATTATCATGGGAAACA 622

Qy 921 TGGCTAAAGCTGTCTTATACTAACGTTACTCTCTGCAAAATAACGATTTCTCATAC 980  
 Db 623 TGAACATTAACCTCTATACTCGTCCTACTCCAGTCAAACTGCAATTCTATTTATA 682

Qy 981 TGGCAGGAGGAACTTGTGGCTTCACACGGGTTCTGGAAACTGGGTTTC 1040  
 Db 683 AGGAAAAGAGACTTAATGGCTTGCCAAACAGATCTGGAAACTGGCTGATTC 742

Qy 1041 TCCPACCAATTCTGGCTCA-----TATGATGATGATGATGATGATGATG 1073  
 Db 743 TTAATACCCATACCTGATGATGATATAACAGATGTCAGTCAATTC 802

Qy 1074 GAAATAACTGCCAGTCGCTTAAAGAGTGTGCGGGAACTGAGTATTGAGTCGACCAA 1133  
 Db 803 AGGAAATTCGAACGCTTGGGCCAAACAAATATCCAAATTCCTGGTTTAAGCCCAA 862

Qy 1134 CTGCGAAATTGGTAAACAGATTATTGGAGCCGAAATTCTCTGGGACTTGTG 1193  
 Db 863 CAAGAAGTGTGGCTGTCAGATGTTGGGAGCCGAAATTCTCTGGCTCTPAGAG 922

Qy 1194 TAAGAGCTTGTGTTATAATGGGGAAACCCAGGGGACATTGACAATAGTAC 1253  
 Db 923 TTGTCCTCTGTGTTAGTTATGGTGTGATGTCGATGGGACTTGTGAAAC 982

Qy 1254 AAGCTGTATAATAATTATGTGTAACCTCTGGAGACTGATGGTATGAAAGGAA 1313  
 Db 983 GTGGATGGCAGCTTGTGACTCTGGGATGTCAGGATGTCAGGATGTCAGG 1042

Qy 1314 AGATGGGTCTCAAACAGATCAAATACTTGTGCAAGCTTGTGCAATGTCGATTTGGGATA 1373  
 Db 1043 AGATGGGTAAAGTGTGCTGCAAAACTGAAAGTAACTTGTGCAAGCTTGTGCTG 1102

Qy 1374 TGGGTTTGTGCTGCAAAACTGAAAGTAACTTGTGCAAGCTTGTGCTG 1433  
 Db 1103 TGGGATTTAACTCAGATACCTGCTGATACTGTCAGTAACTATGCAACAAAGGGCG 1162

Qy 1434 AGTGCACAAACCTTGTGCTGCAAAACTTGTGCAAGCTTGTGCAATGTCGCTG 1493  
 Db 1163 TTGGTCACACCATGATGTTAGCTTGTGCTACTTTGCTAAGAAATAACAGATGTCG 1222

Qy 1494 AGTTTTAAAGTCGAATTATGTTGTGCTGAGGATGAGTGTAGAG 1553  
 Db 1223 ACTTTTGTGAA--TATATTTTGTGAAAGTGGCTCTACTCTGAGA 1279

RESULT 3

US-09-714-865-1.rn1

Sequence 786, Application US/09976594

Patent No. 6673519

GENERAL INFORMATION:

APPLICANT: Furrress, Michael



RESULT 5

US-09-058-489-17

; Sequence 17, Application US/09058489

; Patent No. 6103886

; GENERAL INFORMATION:

; APPLICANT: Whitehead Institute for Biomedical Research

; APPLICANT: Lahn, Bruce

; APPLICANT: Page, David

; TITLE OF INVENTION: Genes in the No. 6103886-Recombinant Region of

; TITLE OF INVENTION: Genes in the Y Chromosome

; FILE REFERENCE: WH197-08PA

; CURRENT APPLICATION NUMBER: US/09/058,489

; CURRENT FILING DATE: 1998-04-10

; EARLIER APPLICATION NUMBER: 60/041,877

; EARLIER FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 17

; LENGTH: 4416

; TYPE: DNA

; ORGANISM: Human

Query Match Score 383 2; DB 3; Length 4416;

Best Local Similarity 58.5%; Pred. No. 3.2e-101;

Matches 761; Conservative 0; Mismatches 503; Indels 36; Gaps 4;

Qy 801 AGACAGGCAAACTGACAHANTAGACACTATCTTCTGGACATGATC 860

Db 529 ACACGGGAAATTGAACTTGTGAAATACTGATGATAACAGAAGCTGGCTCTGGACT 588

Qy 861 CACCAACCAGCAATTCTGACTTTGAGAGTAATCTCTGTCAGACATCAATAACAA 920

Db 589 GTCCTTCACATATGGAATTTGGATGATTGACATGGCAAAATTATGATGGGAACA 648

Qy 921 TTGCTTAAGCTGGTTAACTAGCTTACTCTCTGAAATAACAGTATCTCATAC 980

Db 649 TTGAACTTACTGGCTTACTCTGTCCTTCAACTCCAGTGGAAACATGCTTATTA 708

Qy 981 TTGCAAGGCGGAGATTGATGGCTTCAAAACGGCTCTGGAGAACCTGGGTTC 1040

Db 709 AGGGAAAGAGACTGATGGTGGCCAAACGATCTGGAAACTCAGCAATTCTGG 768

Qy 1041 TCCTTACCAAAATTGGCTCA-----TATGATGCCATGATG 1073

Db 769 TTTTACCCATACTGATGCAAGATAATAACAGATGGTCAAGGTTAGGGTGTGA 828

Qy 1074 GAAATACTGCGCACTGCTGTTAAAGTTGCGGAAACGAGTGTATTTGACGCCA 1133

Db 829 AGGAAATGGAGGTATGGGCCAAACATAATCCAAATTCCTGGTTAGGCCCA 888

Qy 11134 CTCGAGAAATTGGTCACCAAGATTATGGAGGCCAAATTTCCTGGACTGTG 1193

Db 889 CAAAGAAATTGGTCAAGATGAGGAAAGCCAAATTCTACCGATCTAGAG 948

Qy 11194 TAAGAGCTGTTGTTATAATGGGGAAACCAAGCTCAAAATTGAGAAATAGTAC 1253

Db 949 TTGGTCTTGTGTAGTTATGGTGTGTATTTGTCAGGAGTTCTGGACTTA 1008

Db 1069 AGATGGCTCAAAAGATCAAAATCTAGTTGGATGAGCTGATGCAAGGAAA 1313

Db 1009 GTGGATGCCACTGTGTAGTGCCTCAAGAGCTGATGCAAGGGAAA 1068

Qy 1314 AGATTGGCTCAAAAGATCAAAATCTAGTTGGATGAGCTGATGCAAGTGGATA 1373

RESULT 6

US-09-058-489-14

; Sequence 14, Application US/09058489

; Patent No. 6103886

; GENERAL INFORMATION:

; APPLICANT: Whitehead Institute for Biomedical Research

; APPLICANT: Lahn, Bruce

; APPLICANT: Page, David

; TITLE OF INVENTION: Genes in the No. 6103886-Recombinant Region of

; TITLE OF INVENTION: The Y Chromosome

; FILE REFERENCE: WH197-08PA

; CURRENT APPLICATION NUMBER: US/09/058,489

; CURRENT FILING DATE: 1998-04-10

; EARLIER APPLICATION NUMBER: 60/041,877

; EARLIER FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 14

; LENGTH: 3408

; TYPE: DNA

; ORGANISM: Human

US-09-058-489-14



RESULT 8  
US-09-183-706-42  
; Sequence 42, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Faleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATE





RESULT 12  
 US-09-541-681A-1401  
 ; Sequence 1401, Application US/09543681A  
 ; Patent No. 6605719

; GENERAL INFORMATION:  
 ; APPLICANT: GARY BRETON  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709 1002-001  
 ; CURRENT APPLICATION NUMBER: US/09/543,681A  
 ; CURRENT FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,706  
 ; PRIOR FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 8344  
 ; SEQ ID NO 1401  
 ; LENGTH: 1410  
 ; TYPE: DNA  
 ; ORGANISM: Proteus mirabilis  
 US-09-543-681A-1401

Query Match 5.7%; Score 127.6; DB 4; Length 1410;  
 Best Local Similarity 47.1%; Pred. No. 5.8e-27;  
 Matches 514; Conservative 0; Nt smatches 554; Indels 24; Gaps 3;

Db 80 TTTTGAGAAGCTTAATCTGTCAAGACATGCTAAAGCTGGTATAC 939  
 Db 21 TTTCATCGTTGGTTAAGTGAAGCGCTTCCGGTATATGAGCAAGGTAA 80

Query 940 TAAGCTTACCTCTGTCAAATAATAGTATTCCPATACTTCAGGAGATTGAT 999  
 Db 81 AACCCAAACCCCTATCAAACAGCGATTGAGCCGTTGGGTAAGAACGTT 140  
 Db 1000 GGCTGTGCTCAAAAGGGCTGGAAAGCTGCGCTTCTCTACCAATTGGCTCA 1059  
 Db 141 AGCAAGGCAAAAGGTAGGAAAGCCCAATTACATCCAACTGTGAA 200

Query 1060 TATGATGATGATGATAACTGGTCACTTAAAGAGTTGCAAGAACAGGTGAT 1119  
 Db 201 ACTC-----GCTACATGAGCAAGAAAACGAAAGCCGTAAAGCGCT 251  
 Query 1120 TATTGTAGACCAACTCGAGAATGGTCAACCAAGTTATTGGAGCCAGAAATTTC 1179

RESULT 13  
 US-09-557-084-1/C  
 ; Sequence 1, Application US/09557884  
 ; Patent No. 6506581

; GENERAL INFORMATION:  
 ; APPLICANT: Fleischmann et al.  
 ; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue



REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: P1867P1.C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5730

TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match Score 125.6; DB 4;  
 Best Local Similarity 47.3%; Pred. No. 1.3e-24;  
 Matches 506; Conservative 0; Minmatches 54; Indels 30; Gaps 3;

RESULT 15

PCT-US96-05320A-894

/ Sequence 894, Application PC/PCTUS9605320A  
 / GENERAL INFORMATION:  
 / APPLICANT: Human Genome Sciences  
 / ADDRESS: 9410 Key West Avenue  
 / Rockville, MD 20850  
 / APPLICANT: United States of America  
 / APPLICANT: Johns Hopkins University  
 / ADDRESS: 720 Rutland Avenue  
 / Baltimore, MD 21205  
 / APPLICANT: United States of America  
 / APPLICANT: Mark D. Adams  
 / ADDRESS: Owen White  
 / APPLICANT: Hamilton O. Smith  
 / APPLICANT: J. Craig Venter  
 / TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome  
 / NUMBER OF SEQUENCES: 48  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Stern, Kessler, Goldstein & Fox  
 / STREET: 1100 New York Avenue, Suite 600  
 / CITY: Washington  
 / STATE: D.C.  
 / ZIP: 20003-3934  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 / COMPUTER: HP Vectra 486/33  
 / OPERATING SYSTEM: MSDOS version 6.2  
 / SOFTWARE: ASCII text  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: PCTUS96/05320A  
 / FILING DATE: April 22, 1996  
 / CLASSIFICATION:  
 / PRIORITY APPLICATION DATA:  
 / APPLICATION NUMBER: 08/476,102  
 / FILING DATE: June 7, 1995  
 / PRIORITY APPLICATION DATA:  
 / APPLICATION NUMBER: 08/487,429  
 / FILING DATE: June 7, 1995  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Eric K. Steffe  
 / REGISTRATION NUMBER: 36,588  
 / REFERENCE/DOCKET NUMBER: 1488.014PC01  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (301) 371-2600  
 / TELEFAX: (202) 371-2540  
 / INFORMATION FOR SEQ ID NO: 894:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 1254 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: double  
 / TOPOLOGY: linear  
 / PCT-US96-05320A-894

Query Match 5.6\*; Score 123.6; Db 5; Length 1254;  
 Best Local Similarity 47.1\*; Pred. No. 7.9e-16;  
 Matches 495; Conservative 0; Mismatches 539; Indels 18; Gaps 3;  
 Db 1082 TCCCTTGAAAGATAATCGATGAAATTACCA 1113

Qy 921 TGGTAAAGCTGTTTACTAAGCTTACTCTGTGAAATAACGTTATCCATAC 980  
 80 TGGCAAAAGGCTTGTATTGGTACCCATTGGCTTATCCATAC 139

Qy 981 TGGAGACGAAATTATGGTTGCTCAAACAGGTGGAAAGCTGGTTTC 1040  
 Db 140 TAAATGGACGAGATGGCAGAACGCTGAAACTGGTACGGCAAGCATGGTT 199

Qy 1041 TCCATCCAAATTGGCTCATATGATGATGATGGATAAACTGCCATCGTTAAAGAGT 1100  
 Db 200 TACGGCTACTTTCACATCTTAACTCCAAAGA-----TCCATCTTAAT 250

Qy 1101 TCGAGGAACCAAGAGTGTATTGGTACCAACTGGAAATTGGTCAACAGATTATT 1160  
 Db 251 ATCCCTACCCAGAGCTTGTATTGGACCTACTGGAGATTGGTACAGATTAGTA 310

Qy 1161 TGGAGGCAGAAAATTCTTGGACTTGTGAAAGCTGTTTATATGGGGAA 1220  
 Db 311 ATGACGAGAAATTCTGCAAAGCGGTGATTAAAGACGCACTGCTATGGGG 370

Qy 1221 CCCAGCTGGGACATTGCAAAATACTAACGGCTGTAATATATATGCTACTC 1280  
 Db 371 ATGGTATGATAACACTAACGGATTGAGCTGTTGATTTGATGGTACGA 430

Qy 1281 CTGAAAGACTGTGATATCATGGAAAGAAAGTTGGTCTAAACAGATCAAACT 1340  
 Db 431 CGGGCGAGTCATTGATTATGTGAAACAAAGGGTAAATTGTTAGTGAATCGAGT 490

Qy 1341 TAGTTTGGTGAAGCTGATGCCATGGTGGATATGGTTGGTCAAGAAATGAGAAGT 1400  
 Db 491 TCGTGTAGATGAAAGAGATGCAATGTTGACTCGGGTTATCGGTATT 550

Qy 1401 TAATTCTTGTGCCAGGAACTGGCCATCAAAAGAACGCCAAACCTTATGTCAGGCA 1460  
 Db 551 TATTGCTAA-----ATGCCCGTCTCGAAGCTGTTAACGAGTGTATTTCAGCA 604

Qy 1461 CTTTCCAGAGGAATTCAAAGGTGCTGCAAGAATTAAAGTCAAATTATCTGTTG 1520  
 Qy 605 CGTTCTTATAAGTGTGAAATTGCAACCTGAACTGAACTGAACTGAACTGAA -ATATA 661

Qy 1521 TGGCTGTGCAAACTGGTGGAGCTGTGAGATOTTCAGCAACGCTTCAGCTG 1580  
 Db 662 TCGAAATGAAACGAGACAAAACGGCAACGGTAAAGAAGACTTTATCCAT 721

Qy 1581 GCGAGTCTCAAAAGGAAAGACTCTTGAATTTGCAAAACATAGGGATGAAAGAA 1640  
 Db 722 CTAATCGGATAAAATGGCACTTCTTAACCTTAACTGAGATGATGCCCTGAACTG 781

Qy 1641 CTATGGCTTGTGAAACTGAAAGAAAGGAGATTTCATGCCAACTTTCCTTCAAG 1700  
 Db 782 GATTTGTTGGATACTGAAACATGTTGTGAAAGAAATTGGGCTTATTGGGCTG 841

Qy 1701 AAAAATATCAACTAACGATTCCTGTTGAAAGCTGCAACGAGGCGGAGAGCTC 1760  
 Db 842 ATGGCATGTTGCTGTTACTGACTGGGATGACACAAAGTTATGTTAT 901

Qy 1761 TGGAGATTTCGCTTGGAAAGTGCCTGAGTCTGTTGCTACTTCAGTGTGCAAG 1820  
 Db 902 TAAACAAATTATGATGGTGGATATTAACTGGCAACAGATGTTGCTGTTG 961

Qy 1821 GGCTGGATATTGAAATGTCGAAACTGCAATCTTCAATTGATCTCCTTCTPACCAATTGAT 1880  
 Db 962 GCTTGCAATATTCGATGCTGACGATTTCAATTGATGTTACCGATGATCGAAAG 1021

Qy 1881 AATATGTCATGCAATTGGCTGACTGGAAACTGGCAAGGCAATTTCCT 1940  
 Db 1032 ATTATGTCACGAAATTGGCTACTGACGAGCAAGGAAAGTGGTGTTCGATTAGT 1081

Qy 1941 TTTTGTCTGATGATAACCTTAACTGCA 1972